

Pro Arg Ala Ile Arg Thr Arg Tyr Leu Arg Thr Trp Phe Leu Val Asp
165 170 175

Leu Ile Ser Ser Ile Pro Val Asp Tyr Ile Phe Leu Val Val Glu Leu
 180 185 190
 Glu Pro Arg Leu Asp Ala Glu Val Tyr Lys Thr Ala Arg Ala Leu Arg
 195 200 205
 Ile Val Arg Phe Thr Lys Ile Leu Ser Leu Leu Arg Leu Leu Arg Leu
 210 215 220
 Ser Arg Leu Ile Arg Tyr Ile His Gln Trp Glu Glu Ile Phe His Met
 225 230 235 240
 Thr Tyr Asp Leu Ala Ser Ala Val Val Arg Ile Phe Asn Leu Ile Gly
 245 250 255
 Met Met Leu Leu Leu Cys His Trp Asp Gly Cys Leu Gln Phe Leu Val
 260 265 270
 Pro Met Leu Gln Asp Phe Pro Pro Asp Cys Trp Val Ser Ile Asn His
 275 280 285
 Met Val Asn His Ser Trp Gly Arg Gln Tyr Ser His Ala Leu Phe Lys
 290 295 300
 Ala Met Ser His Met Leu Cys Ile Gly Tyr Gly Gln Gln Ala Pro Val
 305 310 315 320
 Gly Met Pro Asp Val Trp Leu Thr Met Leu Ser Met Ile Val Gly Ala
 325 330 335
 Thr Cys Tyr Ala Met Phe Ile Gly His Ala Thr Ala Leu Ile Gln Ser
 340 345 350
 Leu Asp Ser Ser Arg Arg Gln Tyr Gln Glu Lys Tyr Lys Gln Val Glu
 355 360 365
 Gln Tyr Met Ser Phe His Lys Leu Pro Ala Asp Thr Arg Gln Arg Ile
 370 375 380
 His Glu Tyr Tyr Glu His Arg Tyr Gln Gly Lys Met Phe Asp Glu Glu
 385 390 395 400
 Ser Ile Leu Gly Glu Leu Ser Glu Pro Leu Arg Glu Glu Ile Ile Asn
 405 410 415
 Phe Thr Cys Arg Gly Leu Val Ala His Met Pro Leu Phe Ala His Ala
 420 425 430
 Asp Pro Ser Phe Val Thr Ala Val Leu Thr Lys Leu Arg Phe Glu Val
 435 440 445
 Phe Gln Pro Gly Asp Leu Val Val Arg Glu Gly Ser Val Gly Arg Lys
 450 455 460
 Met Tyr Phe Ile Gln His Gly Leu Leu Ser Val Leu Ala Arg Gly Ala
 465 470 475 480
 Arg Asp Thr Arg Leu Thr Asp Gly Ser Tyr Phe Gly Glu Ile Cys Leu
 485 490 495

0076759 0424

Leu Thr Arg Gly Arg Arg Thr Ala Ser Val Arg Ala Asp Thr Tyr Cys
 500 505 510
 Arg Leu Tyr Ser Leu Ser Val Asp His Phe Asn Ala Val Leu Glu Glu
 515 520 525
 Phe Pro Met Met Arg Arg Ala Phe Glu Thr Val Ala Met Asp Arg Leu
 530 535 540
 Leu Arg Ile Gly Lys Lys Asn Ser Ile Leu Gln Arg Lys Arg Ser Glu
 545 550 555 560
 Pro Ser Pro Gly Ser Ser Gly Gly Ile Met Glu Gln His Leu Val Gln
 565 570 575
 His Asp Arg Asp Met Ala Arg Gly Val Arg Gly Arg Ala Pro Ser Thr
 580 585 590
 Gly Ala Gln Leu Ser Gly Lys Pro Val Leu Trp Glu Pro Leu Val His
 595 600 605
 Ala Pro Leu Gln Ala Ala Ala Val Thr Ser Asn Val Ala Ile Ala Leu
 610 615 620
 Thr His Gln Arg Gly Pro Leu Pro Leu Ser Pro Asp Ser Pro Ala Thr
 625 630 635 640
 Leu Leu Ala Arg Ser Ala Trp Arg Ser Ala Gly Ser Pro Ala Ser Pro
 645 650 655
 Leu Val Pro Val Arg Ala Gly Pro Trp Ala Ser Thr Ser Arg Leu Pro
 660 665 670
 Ala Pro Pro Ala Arg Thr Leu His Ala Ser Leu Ser Arg Ala Gly Arg
 675 680 685
 Ser Gln Val Ser Leu Leu Gly Pro Pro Pro Gly Gly Gly Gly Arg Arg
 690 695 700
 Leu Gly Pro Arg Gly Arg Pro Leu Ser Ala Ser Gln Pro Ser Leu Pro
 705 710 715 720
 Gln Arg Ala Thr Gly Asp Gly Ser Pro Gly Arg Lys Gly Ser Gly Ser
 725 730 735
 Glu Arg Leu Pro Pro Ser Gly Leu Leu Ala Lys Pro Pro Arg Thr Ala
 740 745 750
 Gln Pro Pro Arg Pro Pro Val Pro Glu Pro Ala Thr Pro Arg Gly Leu
 755 760 765
 Gln Leu Ser Ala Asn Met
 770

<210> 2

<211> 2325

<212> DNA

<213> Homo sapiens

20250929

<220>

<223> human hyperpolarization-activated voltage-gated
cation channel 3 (HAC3)

<400> 2

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gggcctgagc ctaagaggag gcaccttggg acgctgctcc agcctacggt caacaagtctc 180
tcccttcggg tggtcggcag ccacaaagca gtggaaatcg agcaggagcg ggtgaagtca 240
gcggggggcct ggatcatcca cccctacagc gacttccggg tttactggga cctgatcatg 300
ctgctgctga tgggtgggaa cctcatcgtc ctgctgtgg gcatacctt cttcaaggag 360
gagaactccc cgcttggat cgtcttcaac gtattgtctg atactttctt cctactggat 420
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gccagcctat cccgggcagg gcgctcccg gtctccctgc tgggtccccc tccaggagga 2100
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cagcgggcaa caggcgatgg ctctcctggg cgtaagggat caggaagtga gcggctgcct 2220
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<210> 3

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: amplification
primer

<400> 3

cagccatgga ggcagagcag cggc

<210> 4
 <211> 28
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:amplification
 primer

<400> 4
 ggaggagatc tttcacatga catacgac

28

<210> 5
 <211> 24
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:amplification
 primer

<400> 5
 agtaggatcc atcggtgagg cgtg

24

<210> 6
 <211> 27
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:amplification
 primer

<400> 6
 ttacatgttg gcagaaagct ggagacc

27

<210> 7
 <211> 29
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:degenerate
 amplification primer

<220>
 <221> modified_base
 <222> (24)
 <223> n = g, a, c or t

<400> 7
 tg.gaggaga tcttycayat gacntayga

29

<210> 8
 <211> 27
 <212> DNA
 <213> Artificial Sequence

00763597 012201

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<210> 12
<211> 25
<212> DNA
<213> Artificial Sequence
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			100						105						110
Cys	Arg	Gly	Ala	Ala	Ser	Gly	Pro	Ala	Pro	Gly	Pro	Gly	Pro	Ala	Glu
		115					120					125			
Glu	Ala	Gly	Ser	Glu	Glu	Ala	Gly	Pro	Ala	Gly	Glu	Pro	Arg	Gly	Ser
	130					135					140				
Gln	Ala	Ser	Phe	Met	Gln	Arg	Gln	Phe	Gly	Ala	Leu	Leu	Gln	Pro	Gly
145					150					155					160
Val	Asn	Lys	Phe	Ser	Leu	Arg	Met	Phe	Gly	Ser	Gln	Lys	Ala	Val	Glu
				165					170					175	
Arg	Glu	Gln	Glu	Arg	Val	Lys	Ser	Ala	Gly	Ala	Trp	Ile	Ile	His	Pro
			180					185					190		
Tyr	Ser	Asp	Phe	Arg	Phe	Tyr	Trp	Asp	Phe	Thr	Met	Leu	Leu	Phe	Met
		195					200					205			
Val	Gly	Asn	Leu	Ile	Ile	Ile	Pro	Val	Gly	Ile	Thr	Phe	Phe	Lys	Asp
	210					215					220				
Glu	Thr	Thr	Ala	Pro	Trp	Ile	Val	Phe	Asn	Val	Val	Ser	Asp	Thr	Phe
225					230					235					240
Phe	Leu	Met	Asp	Leu	Val	Leu	Asn	Phe	Arg	Thr	Gly	Ile	Val	Ile	Glu
				245					250					255	
Asp	Asn	Thr	Glu	Ile	Ile	Leu	Asp	Pro	Glu	Lys	Ile	Lys	Lys	Lys	Tyr
			260					265					270		
Leu	Arg	Thr	Trp	Phe	Val	Val	Asp	Phe	Val	Ser	Ser	Ile	Pro	Val	Asp
		275					280					285			
Tyr	Ile	Phe	Leu	Ile	Val	Glu	Lys	Gly	Ile	Asp	Ser	Glu	Val	Tyr	Lys
	290					295					300				
Thr	Ala	Arg	Ala	Leu	Arg	Ile	Val	Arg	Phe	Thr	Lys	Ile	Leu	Ser	Leu
305					310					315					320
Leu	Arg	Leu	Leu	Arg	Leu	Ser	Arg	Leu	Ile	Arg	Tyr	Ile	His	Gln	Trp
				325					330					335	
Glu	Glu	Ile	Phe	His	Met	Thr	Tyr	Asp	Leu	Ala	Ser	Ala	Val	Met	Arg
			340					345					350		
Ile	Cys	Asn	Leu	Ile	Ser	Met	Met	Leu	Leu	Leu	Cys	His	Trp	Asp	Phe
	355						360					365			
Cys	Leu	Gln	Phe	Leu	Val	Pro	Met	Leu	Gln	Asp	Phe	Pro	Arg	Asn	Cys
	370					375					380				
Trp	Val	Ser	Ile	Asn	Gly	Met	Val	Asn	His	Ser	Trp	Ser	Glu	Leu	Tyr
385					390					395					400
Ser	Phe	Ala	Leu	Phe	Lys	Ala	Met	Ser	His	Met	Leu	Cys	Ile	Gly	Tyr
				405					410					415	

Gly	Arg	Gln	Ala	Pro	Glu	Ser	Met	Thr	Asp	Ile	Trp	Leu	Thr	Met	Leu
			420					425					430		
Ser	Met	Ile	Val	Gly	Ala	Thr	Cys	Tyr	Ala	Met	Phe	Ile	Gly	His	Ala
		435					440					445			
Thr	Ala	Leu	Ile	Gln	Ser	Leu	Asp	Ser	Ser	Arg	Arg	Gln	Tyr	Gln	Glu
	450					455					460				
Lys	Tyr	Lys	Gln	Val	Glu	Gln	Tyr	Met	Ser	Phe	His	Lys	Leu	Pro	Ala
465					470					475					480
Asp	Phe	Arg	Gln	Lys	Ile	His	Asp	Tyr	Tyr	Glu	His	Arg	Tyr	Gln	Gly
			485					490						495	
Lys	Met	Phe	Asp	Glu	Asp	Ser	Ile	Leu	Gly	Glu	Leu	Asn	Gly	Pro	Leu
			500					505					510		
Arg	Glu	Glu	Ile	Val	Asn	Phe	Asn	Cys	Arg	Lys	Leu	Val	Ala	Ser	Met
		515					520					525			
Pro	Leu	Phe	Ala	Asn	Ala	Asp	Pro	Asn	Phe	Val	Thr	Ala	Met	Leu	Thr
	530					535					540				
Lys	Leu	Lys	Phe	Glu	Val	Phe	Gln	Pro	Gly	Asp	Tyr	Ile	Ile	Arg	Glu
545					550					555					560
Gly	Thr	Ile	Gly	Lys	Lys	Met	Tyr	Phe	Ile	Glx	His	Gly	Val	Val	Ser
			565						570					575	
Val	Leu	Thr	Lys	Gly	Asn	Lys	Glu	Met	Lys	Leu	Ser	Asp	Gly	Ser	Tyr
			580					585					590		
Phe	Gly	Glu	Ile	Cys	Leu	Leu	Thr	Arg	Gly	Arg	Arg	Thr	Ala	Ser	Val
		595					600					605			
Arg	Ala	Asp	Thr	Tyr	Cys	Arg	Leu	Tyr	Ser	Leu	Ser	Val	Asp	Asn	Phe
	610					615					620				
Asn	Glu	Val	Leu	Glu	Glu	Tyr	Pro	Met	Met	Arg	Arg	Ala	Phe	Glu	Thr
625					630					635					640
Val	Ala	Ile	Asp	Arg	Leu	Asp	Arg	Ile	Gly	Lys	Lys	Asn	Ser	Ile	Leu
				645					650					655	
Leu	His	Lys	Val	Gln	His	Asp	Leu	Asn	Ser	Gly	Val	Phe	Asn	Asn	Gln
			660					665					670		
Glu	Asn	Ala	Ile	Ile	Gln	Glu	Ile	Val	Lys	Tyr	Asp	Arg	Glu	Met	Val
		675					680					685			
Gln	Gln	Ala	Glu	Leu	Gly	Gln	Arg	Val	Gly	Leu	Phe	Pro	Pro	Pro	Pro
		690				695					700				
Pro	Pro	Pro	Gln	Val	Thr	Ser	Ala	Ile	Ala	Thr	Leu	Gln	Gln	Ala	Ala
705					710					715					720
Ala	Met	Ser	Phe	Cys	Pro	Gln	Val	Ala	Arg	Pro	Leu	Val	Gly	Pro	Leu
				725					730					735	

Ala Leu Gly Ser Pro Arg Leu Val Arg Arg Pro Pro Pro Gly Pro Ala
740 745 750

Pro Ala Ala Ala Ser Pro Gly Pro Pro Pro Pro Ala Ser Pro Pro Gly
755 760 765

Ala Pro Ala Ser Pro Arg Ala Pro Arg Thr Ser Pro Tyr Gly Gly Leu
770 775 780

Pro Ala Ala Pro Leu Ala Gly Pro Ala Leu Pro Ala Arg Arg Leu Ser
785 790 795 800

Arg Ala Ser Arg Pro Leu Ser Ala Ser Gln Pro Ser Leu Pro His Gly
805 810 815

Ala Pro Gly Pro Ala Ala Ser Thr Arg Pro Ala Ser Ser Ser Thr Pro
820 825 830

Arg Leu Gly Pro Thr Pro Ala Ala Arg Ala Ala Ala Pro Ser Pro Asp
835 840 845

Arg Arg Asp Ser Ala Ser Pro Gly Ala Ala Gly Gly Leu Asp Pro Gln
850 855 860

Asp Ser Ala Arg Ser Arg Leu Ser Ser Asn Leu
865 870 875

<210> 16

<211> 749

<212> PRT

<213> Homo sapiens

<220>

<223> human hyperpolarization-activated voltage-gated
cation channel 2 (HAC2) missing amino terminus

<400> 16

Lys Glu Gln Glu Arg Val Lys Thr Ala Gly Phe Trp Ile Ile His Pro
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Tyr Ser Asp Phe Arg Phe Tyr Trp Asp Leu Ile Met Leu Ile Met Met
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Val Gly Asn Leu Val Ile Ile Pro Val Gly Ile Thr Phe Phe Thr Glu
35 40 45

Gln Thr Thr Thr Pro Trp Ile Ile Phe Asn Val Ala Ser Asp Thr Val
50 55 60

Phe Leu Leu Asp Leu Ile Met Asn Phe Arg Thr Gly Thr Val Asn Glu
65 70 75 80

Asp Ser Ser Glu Ile Ile Leu Asp Pro Lys Val Ile Lys Met Asn Tyr
85 90 95

Leu Lys Ser Trp Phe Val Val Asp Phe Ile Ser Ser Ile Pro Val Asp
100 105 110

Tyr Ile Phe Leu Ile Val Glu Lys Gly Met Asp Ser Glu Val Tyr Lys
115 120 125

Thr	Ala	Arg	Ala	Leu	Arg	Ile	Val	Arg	Phe	Thr	Lys	Ile	Leu	Ser	Leu	
130							135				140					
Leu	Arg	Leu	Leu	Arg	Leu	Ser	Arg	Leu	Ile	Arg	Tyr	Ile	His	Gln	Trp	
145					150					155					160	
Glu	Glu	Ile	Phe	His	Met	Thr	Tyr	Asp	Leu	Ala	Ser	Ala	Val	Val	Arg	
				165					170					175		
Ile	Phe	Asn	Leu	Ile	Gly	Met	Met	Leu	Leu	Leu	Cys	His	Trp	Asp	Phe	
			180					185					190			
Cys	Leu	Gln	Phe	Leu	Val	Pro	Leu	Leu	Gln	Asp	Phe	Pro	Pro	Asp	Cys	
		195					200					205				
Trp	Val	Ser	Leu	Asn	Glu	Met	Val	Asn	Asp	Ser	Trp	Gly	Lys	Gln	Tyr	
	210					215					220					
Ser	Tyr	Ala	Leu	Phe	Lys	Ala	Met	Ser	His	Met	Leu	Cys	Ile	Gly	Tyr	
225					230					235					240	
Gly	Ala	Gln	Ala	Pro	Val	Ser	Met	Ser	Asp	Leu	Trp	Ile	Thr	Met	Leu	
				245					250					255		
Ser	Met	Ile	Val	Gly	Ala	Thr	Cys	Tyr	Ala	Met	Phe	Val	Gly	His	Ala	
			260					265					270			
Thr	Ala	Leu	Ile	Gln	Ser	Leu	Asp	Ser	Ser	Arg	Arg	Gln	Tyr	Gln	Glu	
		275					280					285				
Lys	Tyr	Lys	Gln	Val	Glu	Gln	Tyr	Met	Ser	Phe	His	Lys	Leu	Pro	Ala	
	290					295					300					
Asp	Met	Arg	Gln	Lys	Ile	His	Asp	Tyr	Tyr	Glu	His	Arg	Tyr	Gln	Gly	
305					310					315					320	
Lys	Ile	Phe	Asp	Glu	Glu	Asn	Ile	Leu	Asn	Glu	Leu	Asn	Asp	Pro	Leu	
				325					330					335		
Arg	Glu	Glu	Ile	Val	Asn	Phe	Asn	Cys	Arg	Lys	Leu	Val	Ala	Thr	Met	
			340					345					350			
Pro	Leu	Phe	Ala	Asn	Ala	Asp	Pro	Asn	Phe	Val	Thr	Ala	Met	Leu	Ser	
		355					360					365				
Lys	Leu	Arg	Phe	Glu	Val	Phe	Gln	Pro	Gly	Asp	Tyr	Ile	Ile	Arg	Glu	
	370					375					380					
Gly	Ala	Val	Gly	Lys	Lys	Met	Tyr	Phe	Ile	Glx	His	Gly	Val	Ala	Gly	
385					390					395					400	
Val	Ile	Thr	Lys	Ser	Ser	Lys	Glu	Met	Lys	Leu	Thr	Asp	Gly	Ser	Tyr	
			405						410					415		
Phe	Gly	Glu	Ile	Cys	Leu	Leu	Thr	Lys	Gly	Arg	Arg	Thr	Ala	Ser	Val	
			420					425					430			
Arg	Ala	Asp	Thr	Tyr	Cys	Arg	Leu	Tyr	Ser	Leu	Ser	Val	Asp	Asn	Phe	
		435					440					445				

Asn Glu Val Leu Glu Glu Tyr Pro Met Met Arg Arg Ala Phe Glu Thr
 450 455 460
 Val Ala Ile Asp Arg Leu Asp Arg Ile Gly Lys Lys Asn Ser Ile Leu
 465 470 475 480
 Leu Gln Lys Phe Gln Lys Asp Leu Asn Thr Gly Val Phe Asn Asn Gln
 485 490 495
 Glu Asn Glu Ile Leu Lys Gln Ile Val Lys His Asp Arg Glu Met Val
 500 505 510
 Gln Ala Ile Ala Pro Ile Asn Tyr Pro Gln Met Thr Thr Leu Asn Ser
 515 520 525
 Thr Ser Ser Thr Thr Thr Pro Thr Ser Arg Met Arg Thr Gln Ser Pro
 530 535 540
 Pro Val Tyr Thr Ala Thr Ser Leu Ser His Ser Asn Leu His Ser Pro
 545 550 555 560
 Ser Pro Ser Thr Gln Thr Pro Gln Pro Ser Ala Ile Leu Ser Pro Cys
 565 570 575
 Ser Tyr Thr Thr Ala Val Cys Ser Pro Pro Val Gln Ser Pro Leu Ala
 580 585 590
 Ala Arg Thr Phe His Tyr Ala Ser Pro Thr Ala Ser Gln Leu Ser Leu
 595 600 605
 Met Gln Gln Gln Pro Gln Gln Gln Val Gln Gln Ser Gln Pro Pro Gln
 610 615 620
 Arg Gln Pro Gln Gln Pro Ser Pro Gln Pro Gln Thr Pro Gly Ser Ser
 625 630 635 640
 Thr Pro Lys Asn Glu Val His Lys Ser Thr Gln Ala Leu His Asn Thr
 645 650 655
 Asn Leu Thr Arg Glu Val Arg Pro Phe Ser Ala Trp Gln Pro Ser Leu
 660 665 670
 Pro His Glu Val Ser Thr Leu Ile Ser Arg Pro His Pro Thr Val Gly
 675 680 685
 Glu Ser Leu Ala Ser Ile Pro Gln Pro Val Thr Ala Val Pro Gly Thr
 690 695 700
 Gly Leu Gln Ala Gly Gly Arg Ser Thr Val Pro Gln Arg Val Thr Phe
 705 710 715 720
 Phe Arg Gln Met Ser Ser Gly Ala Ile Pro Pro Asn Arg Gly Val Leu
 725 730 735
 Pro Ala Pro Leu Pro Leu Ile Thr Pro His Pro Lys Lys
 740 745

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